



Sequence Listing.ST25.txt
SEQUENCE LISTING

RECEIVED
JAN 03 2001
TECH CENTER 1600/2900

<110> Pfizer Inc.
Fidock, Mark David

<120> Enzyme PDE xiv

<130> PC10315AGPR

<160> 26

<170> PatentIn version 3.0

<210> 1

<211> 446

<212> PRT

<213> Mouse

<400> 1

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1 5 10 15

Pro Glu Gln Ser Val Lys Cys Val Cys Met Leu Gly Asp Val Arg Leu
20 25 30

Arg Gly Gln Thr Gly Val Pro Ala Glu Arg Arg Gly Ser Tyr Pro Phe
35 40 45

Ile Asp Phe Arg Leu Leu Asn Asn Thr Thr His Ser Gly Glu Ile Gly
50 55 60

Thr Lys Lys Lys Val Lys Arg Leu Leu Ser Phe Gln Arg Tyr Phe His
65 70 75 80

Ala Ser Arg Leu Leu Arg Gly Ile Ile Pro Gln Ala Pro Leu His Leu
85 90 95

Leu Asp Glu Asp Tyr Leu Gly Gln Ala Arg His Met Leu Ser Lys Val
100 105 110

Gly Thr Trp Asp Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly
115 120 125

Asn Ser Leu Val Thr Leu Leu Cys His Leu Phe Asn Ser His Gly Leu
130 135 140

Ile His His Phe Lys Leu Asp Met Val Thr Leu His Arg Phe Leu Val
145 150 155 160

Met Val Gln Glu Asp Tyr His Gly His Asn Pro Tyr His Asn Ala Val
165 170 175

Sequence Listing.ST25.txt

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His Ala Ala Asp Val Thr Gln Ala Met His Cys Tyr Leu Lys Glu Pro
180                               185                               190

Lys Leu Ala Ser Phe Leu Thr Pro Leu Asp Ile Met Leu Gly Leu Leu
195                               200                               205

Ala Ala Ala Ala His Asp Val Asp His Pro Gly Val Asn Gln Pro Phe
210                               215                               220

Leu Ile Lys Thr Asn His His Leu Ala Asn Leu Tyr Gln Asn Met Ser
225                               230                               235                               240

Val Leu Glu Asn His His Trp Arg Ser Thr Ile Gly Met Leu Arg Glu
245                               250                               255

Ser Arg Leu Leu Ala His Leu Pro Lys Glu Met Thr Gln Asp Ile Glu
260                               265                               270

Gln Gln Leu Gly Ser Leu Ile Leu Ala Thr Asp Ile Asn Arg Gln Asn
275                               280                               285

Glu Phe Leu Thr Arg Leu Lys Ala His Leu His Asn Lys Asp Leu Arg
290                               295                               300

Leu Glu Asn Val Gln Asp Arg His Phe Met Leu Gln Ile Ala Leu Lys
305                               310                               315                               320

Cys Ala Asp Ile Cys Asn Pro Cys Arg Ile Trp Glu Met Ser Lys Gln
325                               330                               335

Trp Ser Glu Arg Val Cys Glu Glu Phe Tyr Arg Gln Gly Asp Leu Glu
340                               345                               350

Gln Lys Phe Glu Leu Glu Ile Ser Pro Leu Cys Asn Gln Gln Lys Asp
355                               360                               365

Ser Ile Pro Ser Ile Gln Ile Gly Phe Met Thr Tyr Ile Val Glu Pro
370                               375                               380

Leu Phe Arg Glu Trp Ala Arg Phe Thr Gly Asn Ser Thr Leu Ser Glu
385                               390                               395                               400

Asn Met Leu Ser His Leu Ala His Asn Lys Ala Gln Trp Lys Ser Leu
405                               410                               415

Leu Ser Asn Gln His Arg Arg Arg Gly Ser Gly Gln Asp Leu Ala Gly
420                               425                               430

Pro Ala Pro Glu Thr Leu Glu Gln Thr Glu Gly Ala Thr Pro
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<210> 2
<211> 1341

Sequence Listing.ST25.txt

<212> DNA

<213> Mouse

<400> 2

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gaacgccgtg gctcctaccc attcattgac ttccgtctac ttaacaatac aacacactca	180
ggggaaattg gcaccaagaa aaaggtgaaa cgactgttaa gtttccaaag atacttccat	240
gcatctaggc ttctccgggg gattataccg caggcccctc tccacctgct ggatgaagac	300
taccttggac aagcaaggca catgctctcc aaagttggaa cgtgggactt tgacattttc	360
ttgtttgatc gcttgacaaa tgggaacagt ctggtaactc tgttgtgtca cctcttcaac	420
tcccatgggc tcatccacca tttcaagctc gatatggtga ccttgcacag gtttctggtt	480
atggttcagg aagattacca cggtcacaac ccataccaca atgctgttca cgcagccgac	540
gtcaccacagg ccatgcactg ttacctgaag gagccaaagt tggcaagctt cctcacacct	600
ctggacatca tgcttgact actggctgca gcagctcatg acgtggacca cccaggggtc	660
aaccagccat ttttgatcaa aactaaccac catcttgcca acctgtatca gaatatgtct	720
gtactggaga atcaccactg gcgatctaca attggcatgc ttcgagaatc acggctcctg	780
gctcacttgc caaaggaaat gacacaggat atcgaacagc agctgggctc cctcatcttg	840
gccacggata tcaacagaca gaatgagttt ctgaccgct taaaagctca cctccacaat	900
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aacatgctaa gccatctcgc gcacaacaaa gccagtgga agagcctgct gtccaatcag	1260
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<210> 3

<211> 288

Sequence Listing.ST25.txt

<212> PRT

<213> Human

<400> 3

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Arg	Gly	Gln	Thr	Gly	Val	Arg	Ala	Glu	Arg	Arg	Gly	Ser	Tyr	Pro	Phe	35	40	45	
Ile	Asp	Phe	Arg	Leu	Leu	Asn	Ser	Thr	Thr	Tyr	Ser	Gly	Glu	Ile	Gly	50	55	60	
Thr	Lys	Lys	Lys	Val	Lys	Arg	Leu	Leu	Ser	Phe	Gln	Arg	Tyr	Phe	His	65	70	75	80
Ala	Ser	Arg	Leu	Leu	Arg	Gly	Ile	Ile	Pro	Gln	Ala	Pro	Leu	His	Leu	85	90	95	
Leu	Asp	Glu	Asp	Tyr	Leu	Gly	Gln	Ala	Arg	His	Met	Leu	Ser	Lys	Val	100	105	110	
Gly	Met	Trp	Asp	Phe	Asp	Ile	Phe	Leu	Phe	Asp	Arg	Leu	Thr	Asn	Gly	115	120	125	
Asn	Ser	Leu	Val	Thr	Leu	Leu	Cys	His	Leu	Phe	Asn	Thr	His	Gly	Leu	130	135	140	
Ile	His	His	Phe	Lys	Leu	Asp	Met	Val	Thr	Leu	His	Arg	Phe	Leu	Val	145	150	155	160
Met	Val	Gln	Glu	Asp	Tyr	His	Ser	Gln	Asn	Pro	Tyr	His	Asn	Ala	Val	165	170	175	
His	Ala	Ala	Asp	Val	Thr	Gln	Ala	Met	His	Cys	Tyr	Leu	Lys	Glu	Pro	180	185	190	
Lys	Leu	Ala	Ser	Phe	Leu	Thr	Pro	Leu	Asp	Ile	Met	Leu	Gly	Leu	Leu	195	200	205	
Ala	Ala	Ala	Ala	His	Asp	Val	Asp	His	Pro	Gly	Val	Asn	Gln	Pro	Phe	210	215	220	
Leu	Ile	Lys	Thr	Asn	His	His	Leu	Ala	Asn	Leu	Tyr	Gln	Asn	Met	Ser	225	230	235	240
Val	Leu	Glu	Asn	His	His	Trp	Arg	Ser	Thr	Ile	Gly	Met	Leu	Arg	Glu	245	250	255	

Sequence Listing.ST25.txt

Ser Arg Leu Leu Ala His Leu Pro Lys Glu Met Thr Gly Thr Trp Asp
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Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly Asn Ser Leu Val
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<210> 4
<211> 807
<212> DNA
<213> Human

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gaacgccgtg gctcctaccc attcattgac ttccgcctac ttaacagtac aacataactca 180
ggggagattg gcaccaagaa aaaggtgaaa agactattaa gctttcaaag atacttccat 240
gcatcaaggc tgcttcgtgg aattatacca caagcccctc tgcacctgct ggatgaagac 300
taccttggac aagcaaggca tatgctctcc aaagtgggaa tgtgggattt tgacattttc 360
ttgtttgatc gcttgacaaa tggaaacagc ctggtaacac tggttgacca cctcttcaat 420
acccatggac tcattcacca tttcaagtta gatatgggtga ccttacaccg atttttagtc 480
atggttcaag aagattacca cagccaaaac ccgtatcaca atgctgttca cgcagccgac 540
gtcaccagc ccatgcactg ctacctgaaa gagccaaagc ttgccagctt cctcacgcct 600
ctggacatca tgcttgact gctggctgca gcagcacacg atgtggacca cccaggggtg 660
aaccagccat ttttgataaa aactaaccac catcttgcaa acctatatca gaatatgtct 720
gtgctggaga atcatcactg gcgatctaca attggcatgc ttcgagaatc aaggcttctt 780
gctcatttgc caaaggaaat gacgtaa 807

<210> 5
<211> 450
<212> PRT
<213> Human

<400> 5

Met Ser Cys Leu Met Val Glu Arg Cys Gly Glu Ile Leu Phe Glu Asn
1 5 10 15

Pro Asp Gln Asn Ala Lys Cys Val Cys Met Leu Gly Asp Ile Arg Leu
20 25 30

Sequence Listing.ST25.txt

Arg	Gly	Gln	Thr	Gly	Val	Arg	Ala	Glu	Arg	Arg	Gly	Ser	Tyr	Pro	Phe	
		35					40					45				
Ile	Asp	Phe	Arg	Leu	Leu	Asn	Ser	Thr	Thr	Tyr	Ser	Gly	Glu	Ile	Gly	
	50					55					60					
Thr	Lys	Lys	Lys	Val	Lys	Arg	Leu	Leu	Ser	Phe	Gln	Arg	Tyr	Phe	His	
65					70					75					80	
Ala	Ser	Arg	Leu	Leu	Arg	Gly	Ile	Ile	Pro	Gln	Ala	Pro	Leu	His	Leu	
				85					90					95		
Leu	Asp	Glu	Asp	Tyr	Leu	Gly	Gln	Ala	Arg	His	Met	Leu	Ser	Lys	Val	
			100				105						110			
Gly	Met	Trp	Asp	Phe	Asp	Ile	Phe	Leu	Phe	Asp	Arg	Leu	Thr	Asn	Gly	
		115					120					125				
Asn	Ser	Leu	Val	Thr	Leu	Leu	Cys	His	Leu	Phe	Asn	Thr	His	Gly	Leu	
	130					135					140					
Ile	His	His	Phe	Lys	Leu	Asp	Met	Val	Thr	Leu	His	Arg	Phe	Leu	Val	
145					150					155					160	
Met	Val	Gln	Glu	Asp	Tyr	His	Ser	Gln	Asn	Pro	Tyr	His	Asn	Ala	Val	
				165					170					175		
His	Ala	Ala	Asp	Val	Thr	Gln	Ala	Met	His	Cys	Tyr	Leu	Lys	Glu	Pro	
			180					185					190			
Lys	Leu	Ala	Ser	Phe	Leu	Thr	Pro	Leu	Asp	Ile	Met	Leu	Gly	Leu	Leu	
		195					200					205				
Ala	Ala	Ala	Ala	His	Asp	Val	Asp	His	Pro	Gly	Val	Asn	Gln	Pro	Phe	
	210					215					220					
Leu	Ile	Lys	Thr	Asn	His	His	Leu	Ala	Asn	Leu	Tyr	Gln	Asn	Met	Ser	
225					230					235					240	
Val	Leu	Glu	Asn	His	His	Trp	Arg	Ser	Thr	Ile	Gly	Met	Leu	Arg	Glu	
				245					250					255		
Ser	Arg	Leu	Leu	Ala	His	Leu	Pro	Lys	Glu	Met	Thr	Gln	Asp	Ile	Glu	
		260						265					270			
Gln	Gln	Leu	Gly	Ser	Leu	Ile	Leu	Ala	Thr	Asp	Ile	Asn	Arg	Gln	Asn	
		275					280					285				
Glu	Phe	Leu	Thr	Arg	Leu	Lys	Ala	His	Leu	His	Asn	Lys	Asp	Leu	Arg	
	290					295					300					
Leu	Glu	Asp	Ala	Gln	Asp	Arg	His	Phe	Met	Leu	Gln	Ile	Ala	Leu	Lys	

Sequence Listing.ST25.txt

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305                               310                               315                               320
Cys Ala Asp Ile Cys Asn Pro Cys Arg Ile Trp Glu Met Ser Lys Gln
                      325                               330                               335
Trp Ser Glu Arg Val Cys Glu Glu Phe Tyr Arg Gln Gly Glu Leu Glu
                      340                               345                               350
Gln Lys Phe Glu Leu Glu Ile Ser Pro Leu Cys Asn Gln Gln Lys Asp
                      355                               360                               365
Ser Ile Pro Ser Ile Gln Ile Gly Phe Met Ser Tyr Ile Val Glu Pro
                      370                               375                               380
Leu Phe Arg Glu Trp Ala His Phe Thr Gly Asn Ser Thr Leu Ser Glu
385                               390                               395                               400
Asn Met Leu Gly His Leu Ala His Asn Lys Ala Gln Trp Lys Ser Leu
                      405                               410                               415
Leu Pro Arg Gln His Arg Ser Arg Gly Ser Ser Gly Ser Gly Pro Asp
                      420                               425                               430
His Asp His Ala Gly Gln Gly Thr Glu Ser Glu Glu Gln Glu Gly Asp
                      435                               440                               445
Ser Pro
450

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<210> 6
<211> 1353
<212> DNA
<213> Human

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gaacgccgtg gtcctaccc attcattgac ttccgcctac ttaacagtac aacataactca      180
ggggagattg gcaccaagaa aaaggtgaaa agactattaa gctttcaaag atacttccat      240
gcatcaaggc tgcttcgtgg aattatacca caagcccctc tgcacctgct ggatgaagac      300
taccttggac aagcaaggca tatgctctcc aaagtgggaa tgtgggattt tgacattttc      360
ttgtttgatc gcttgacaaa tggaaacagc ctggtaacac tgttgtgcca cctcttcaat      420
acccatggac tcattcacca tttcaagtta gatatggtga ccttacaccg atttttagtc      480
atggttcaag aagattacca cagccaaaac ccgtatcaca atgctgttca cgcagccgac      540

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Sequence Listing.ST25.txt

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aaccagccat ttttgataaa aactaaccac catcttgcaa acctatatca gaatatgtct      720
gtgctggaga atcatcactg gcgatctaca attggcatgc ttcgagaatc aaggcttctt      780
gctcatttgc caaaggaaat gacacaggat attgaacagc agctgggctc cttgatcttg      840
gcaacagaca tcaacaggca gaatgaattt ttgaccagat tgaaagctca cctccacaat      900
aaagacttaa gactggagga tgcacaggac aggcacttta tgcttcagat cgccttgaag      960
tgtgtgaca tttgcaatcc ttgtagaatc tgggagatga gcaagcagtg gagtgaagg      1020
gtctgtgaag aattctacag gcaaggtgaa cttgaacaga aatttgaact ggaaatcagt      1080
cctctttgta atcaacagaa agattccatc cctagtatac aaattggttt catgagctac      1140
atcgtggagc cgctcttccg ggaatgggcc catttcacgg gtaacagcac cctgtcggag      1200
aacatgctgg gccacctcgc acacaacaag gcccagtgga agagcctggt gcccaggcag      1260
cacagaagca ggggcagcag tggcagcggg cctgaccacg accacgcagg ccaagggact      1320
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<210> 7
<211> 2823
<212> DNA
<213> Mouse

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<400> 7
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ttaaagtgtc tgtttaatgg ttgagaggtg tggcgaagtc ttgtttgaga gccctgaaca      480
gagtggtcaaa tgtgtttgca tgctaggaga tgtacgacta aggggtcaga cgggggttcc      540

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Sequence Listing.ST25.txt

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cgacgtcacc	caggccatgc	actgttacct	gaaggagcca	aagttggcaa	gcttcctcac	1020
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Sequence Listing.ST25.txt

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 <211> 2992
 <212> DNA
 <213> Human

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tcttgtttaa tggttgagag gtgtggcgaa atcttgtttg agaaccccga tcagaatgcc	360
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gagattggca ccaagaaaaa ggtgaaaaga ctattaagct ttcaaagata cttccatgca	540
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Sequence Listing.ST25.txt

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gttcaagaag attaccacag ccaaaacccg tatcacaatg ctgttcacgc agccgacgtc	840
accagggcca tgcaactgcta cctgaaagag ccaaagcttg ccagcttcct cacgcctctg	900
gacatcatgc ttggactgct ggctgcagca gcacacgatg tggaccaccc aggggtgaac	960
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Sequence Listing.ST25.txt

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Met Leu Ser Lys Val Gly
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20 25 30

Asp Ile Met Leu Gly Leu Leu Ala Ala Ala Ala His Asp Val Asp His
35 40 45

Pro Gly Val Asn Gln Pro Phe Leu Ile Lys Thr Asn His His Leu Ala
50 55 60

Asn Leu Tyr Gln Asn Met Ser Val Leu Glu Asn His His Trp Arg Ser
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Sequence Listing.ST25.txt

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 Lys Asp Ser Ile Pro Ser Ile Gln Ile Gly Phe Met
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Sequence Listing.ST25.txt

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22